```
      (FILE 'HOME' ENTERED AT 15:42:34 ON 25 APR 2003)

      FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
      ENTERED AT 15:43:02 ON 25 APR 2003
L1        2199 S SHOSHAN A?/AU OR WASSERMAN A?/AU OR MINTZ E?/AU OR MINTZ
L?/A
L2          17 S L1 AND TRANSCRIPTOME#
L3           6 DUP REM L2 (11 DUPLICATES REMOVED)
L4        2405 S TRANSCRIPTOME#
L5          14 S L4 AND (SPLIC? VARIANT#)
L6          60 S L4 AND MRNA TRANSCRIPT#
L7         306 S L4 AND LIBRAR###
L8          44 S L7 AND MICROARRAY
L9           0 S L4 AND OLGIONUCLEOTIDES
L10          7 DUP REM L5 (7 DUPLICATES REMOVED)
L11         14 DUP REM L6 (46 DUPLICATES REMOVED)
L12         25 DUP REM L8 (19 DUPLICATES REMOVED)
L13          6 S (L10 OR L11) AND (MICROARRAY OR CHIP OR GLASS SUPPORT)

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ACCESSION NUMBER: 2001:519168 BIOSIS
DOCUMENT NUMBER: PREV200100519168
TITLE: DNA chips designed to detect alternative splicing using
                      LEADS.

AUTHOR(S):   Wasserman, Alon (1); Shoshan, Avi (1); Grebinskiy,
Vladimir
                      (1)
CORPORATE SOURCE: (1) Compugen Inc., Jamesburg, NJ USA
SOURCE: International Genome Sequencing and Analysis Conference,
                      (2000) Vol. 12, pp. 63. print.
                      Meeting Info.: 12th International Genome Sequencing and
                      Analysis Conference Miami Beach, Florida, USA September
                      12-15, 2000
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB   We design chips enabling the detection of alternative **splice
      variants**. The design optimally chooses segments representing the
      splice variants of each gene. Probes are selected from
      each segment using criteria including specificity, distance from the 3'
      end, sequence quality, GC content, and so on. The designs are based on
the
      LEADS software that clusters and assembles ESTs, known mRNAs and genomic
      data. For each gene, it produces a list of predicted **mRNA
      transcripts**, each a different **splice variant**.
      Multiply covered areas are used to detect and eliminate sequencing
errors.
      These areas are also used for the detection of polymorphisms, which can
be
      used in genotyping chips. Having good designs is crucial to extract
      meaningful information from **chip** experiments. Designs not using
      all available data, **splice variants** and sequencing
      errors might lead to useless probes and misleading results. It is
believed
      that at least 35% of human genes have alternative **splice
      variants**, and it is important to distinguish between their
      expression patterns. This is achieved by choosing probes that are unique
      to some of the variants. If one just wishes to measure the overall
      expression level of the gene, probes that are common to all the variants
      can be chosen.

138:164702
TITLE: Method and system for identifying **splice**
                               variants of a gene
INVENTOR(S):   Bingham, Jonathan; Srinivasan, Subha
PATENT ASSIGNEE(S):   Jivan Biologics, Inc., USA
SOURCE: PCT Int. Appl., 28 pp.
                               CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

          PATENT NO.   KIND   DATE   APPLICATION NO.   DATE
          ---------------   ----   --------   ----------------   --------
          WO 2003014295   A2   20030220   WO 2002-US23819   20020725
               W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
                   CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
                   GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
                   LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
                   PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
                   UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
                   TJ, TM
               RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
                   CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
                   PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
                   NE, SN, TD, TG
PRIORITY APPLN. INFO.:   US 2001-307911P   P   20010725
                                             US 2001-329914P   P   20011017
                                             US 2001-343269P   P   20011221
                                             US 2001-343286P   P   20011221
                                             US 2001-343298P   P   20011221
                                             US 2002-146720   A   20020514

AB   A method and system for identifying mRNA present in a sample. A
     splice variant technique selects a set of possible
     exon-exon junctions based on exons of expected **mRNA
     transcripts**. The **splice variant** technique
     then selects indicator polynucleotides for the exon-exon junctions and
     detects the expression level of the indicator polynucleotides in the
     sample. The **splice variant** technique then may use a
     math. algorithm to identify possible **splice variants**
     in the sample from the obsd. expression levels. The math. algorithm may
     be an algorithm for solving linear equations, a least squares algorithm,
     or any other algorithm for finding a possible soln. for a set of
     equations. The **splice variant** technique may also
     detect the expression levels of the exons themselves to provide more
     information for use in identifying the **splice variants**
     in the sample. The **splice variant** technique detects
     the expression levels of the exons by selecting indicator polynucleotides
     for the exons and designing probes to detect the expression level of the
     indicator polynucleotides (and thus the exons themselves) in the sample
     using the nucleotide array technol.

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L?/A
L2          17 S L1 AND TRANSCRIPTOME#
L3           6 DUP REM L2 (11 DUPLICATES REMOVED)
L4        2405 S TRANSCRIPTOME#
L5          14 S L4 AND (SPLIC? VARIANT#)
L6          60 S L4 AND MRNA TRANSCRIPT#
L7         306 S L4 AND LIBRAR###
L8          44 S L7 AND MICROARRAY
L9           0 S L4 AND OLGIONUCLEOTIDES
L10          7 DUP REM L5 (7 DUPLICATES REMOVED)
L11         14 DUP REM L6 (46 DUPLICATES REMOVED)
L12         25 DUP REM L8 (19 DUPLICATES REMOVED)
L13          6 S (L10 OR L11) AND (MICROARRAY OR CHIP OR GLASS SUPPORT)
L14      21275 S MRNA TRANSCRIPT#
L15        311 S L14 AND SPLICE VARIANT#
L16         35 S L15 AND (OLIGONUCLEOTIDE LIBRAR### OR LIBRAR###)
L17          7 S L15 AND (MICROARRAY OR CHIP OR GLASS SUPPORT)
L18         14 DUP REM L16 (21 DUPLICATES REMOVED)
L19          6 DUP REM L17 (1 DUPLICATE REMOVED)

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